

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2005, 10:07:30 ; Search time 174 Seconds  
(without alignments)  
182.465 Million cell updates/sec

Title: US-10-672-108-6

Perfect score: 336

Sequence: 1 MTTVKILNGTKLGETTTE.....EWTYDDATKTFVTVEHHHH 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_Q3:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285	84.8	455	2 Q53291	peptostrept
2	284	84.5	185	2 Q54181	streptococc
3	284	84.5	593	1 SPG2_STRSG	streptococc
4	281	83.6	448	1 SPG1_STRSG	streptococc
5	264	78.6	60	2 Q53337	streptococc
6	261	77.7	413	2 Q53974	streptococc
7	261	77.7	664	2 Q53975	streptococc
8	257	76.5	569	2 Q93EM8	streptococc
9	220	65.5	429	2 Q56212	streptococc
10	220	65.5	433	2 Q76K19	streptococc
11	128.5	38.2	573	2 Q56192	staphylococ
12	127.5	37.9	492	2 Q56193	staphylococ
13	75	22.3	412	2 Q8YLV7	oryza sativ
14	74	22.0	1965	2 P7J089	synchocyst
15	69	20.5	148	2 Q7N736	photorhabd
16	68.5	20.4	736	1 EF2_SULTO	sulfolobus
17	68	20.2	1020	2 Q9KG76	bacillus ha
18	67	19.9	735	2 Q6TM49	bacterioph
19	67	19.9	1010	2 Q88XH5	lactobacill
20	66.5	19.8	452	2 Q8FMT2	corynebacte
21	66	19.6	413	2 Q9N8L7	trypanosoma
22	66	19.6	644	2 Q9VXA3	drosophila
23	66	19.6	3930	2 Q98E20	rhizobium l
24	66	19.6	8173	2 Q7UDU8	rhodospirell
25	65	19.3	167	2 Q722L3	bacillus ce
26	65	19.3	585	2 Q649K0	uncultured
27	65	19.3	1062	2 Q6C4K7	yarrowia li
28	65	19.3	1256	2 Q6D875	erwinia car
29	64.5	19.2	132	2 Q838Z7	enterococcu
30	64.5	19.2	148	1 FUR_YERPE	versinia pe
31	64.5	19.2	279	2 Q8FLY7	corynebacte

32 64.5 19.2 736 1 EF2\_SULAC P23112 sulfolobus  
33 64 19.0 240 2 Q89RX0 Q89RX0 bradyrhizob  
34 64 19.0 410 2 Q6NIX7 Q6NIX7 corynebacte  
35 64 19.0 1081 2 Q68831 Q68831 bacteroides  
36 64 19.0 2596 2 Q75D43 Q75D43 ashbya goss  
37 63.5 18.9 308 2 Q9PPG7 Q9PPG7 campylobact  
38 63.5 18.9 474 2 Q6AVU2 Q6AVU2 oryza sativ  
39 63 18.8 148 2 Q99T18 Q99T18 staphylococ  
40 63 18.8 148 2 Q7A0J4 Q7A0J4 staphylococ  
41 63 18.8 148 2 Q7A4T8 Q7A4T8 staphylococ  
42 63 18.8 148 2 Q9RL3 Q9RL3 staphylococ  
43 63 18.8 148 2 Q6G873 Q6G873 staphylococ  
44 63 18.8 148 2 Q6GFU6 Q6GFU6 staphylococ  
45 63 18.8 150 2 Q8C9Q7 Q8C9Q7 staphylococ

## ALIGNMENTS

RESULT 1  
Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.  
AC Q53291, 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Protein LG (Fragment).  
OS Peptostreptococcus magnus.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales;  
OC Peptostreptococcaceae; Finegoldia.  
OX NCBI\_TaxID=1260;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91094283; PubMed=1460053;  
RA Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.:  
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties.";  
RL J. Biol. Chem. 267:25583-25588(1992).  
DR EMBL; S50809; AAA03280.1; --  
DR HSSP; Q51912; 2PTL  
DR GO; GO:0005618; C:cell wall; IEA.  
DR GO; GO:0005515; P:protein binding; IEA.  
DR InterPro; IPR003147; BI.  
DR InterPro; IPR000724; IGG\_bind\_B.  
DR Pfam; PF02246; BL; 4.  
DR Pfam; PF01378; IGG\_binding\_B; 2.  
FT NON\_TER 455 455  
SQ SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64;  
Query Match 84.8%; Score 285; DB 2; Length 455;  
Best Local Similarity 96.5%; Pred. No. 1.8e-23;  
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MTTVKILNGTKLGETTTEAADAATAKVPKQVANDGVGDGWTYDDATKTFVTVE 57  
Db 328 MDTVKILNGTKLGETTTEAADAATAKVPKQVANDGVGDGWTYDDATKTFVTVE 384  
RESULT 2  
Q54181 ID Q54181 PRELIMINARY; PRT; 185 AA.  
AC Q54181, 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Protein G'.  
GN Name=Protein G' gene;  
OS Streptococcus sp. (Lancefield group G).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1320;  
RN [1]  
RP SEQUENCE FROM N.A.



371 VTYKLKLVINGKTLKGETTTEAVDAATAEKVKFYQYANDNGVDGWTYYDDATKTFVTVE 427

Db

## RESULT 4

SPGL\_STRSG STANDARD; PRT; 448 AA.  
AC P06654;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Immunoglobulin G binding protein G precursor (IgG binding protein G).  
GN Name:spg;  
OS Streptococcus sp. (Lancefield group G).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus  
OX NCBI\_TaxID=1320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86304178; PubMed=3745123;  
RA Fahnestock S.R., Alexander P., Nagle J., Filpula D.;  
RT "Gene for an immunoglobulin-binding protein from a group G  
streptococcus";  
RL J. Bacteriol. 167:870-880(1986).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS) OF 228-282.  
RX MEDLINE=94213848; PubMed=8161530;  
RA Gallagher T., Alexander P., Bryan P., Gilliland G.L.;  
RT "Two crystal structures of the B1 immunoglobulin-binding domain of  
streptococcal protein G and comparison with NMR.";  
RL Biochemistry 33:4721-4729(1994).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 293-351.  
RX MEDLINE=95055731; PubMed=7966308;  
RA Derrick J.F., Wigley D.B.;  
RT "The third IgG-binding domain from streptococcal protein G. An  
analysis by X-ray crystallography of the structure alone and in a  
complex with Fab.";  
RL J. Mol. Biol. 243:906-918(1994).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 297-352.  
RX MEDLINE=95308043; PubMed=7788293; DOI=10.1016/S0969-2126(01)00157-5;  
RA Sauer-Eriksson A.E., Kleywegt G.J., Jones T.A.;  
RT "Crystal structure of the C2 fragment of streptococcal protein G in  
complex with the Fc domain of human IgG";  
RL Structure 3:265-278(1995).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 228-282.  
RA Butterworth S., Lamzin V.S., Wigley D.B., Derrick J.P., Wilson K.S.;  
RT Submitted (APR-1997) to the PDB data bank.  
RN [6]  
RP STRUCTURE BY NMR OF 298-351.  
RX MEDLINE=91335209; PubMed=1871600;  
RA Gronenborn A.M., Filpula D.R., Essig N.Z., Achari A., Whitlow M.,  
RA Wingfield P.T., Clore G.M.;  
RT "A novel, highly stable fold of the immunoglobulin binding domain of  
streptococcal protein G";  
RL Science 253:657-661(1991).  
CC -!- FUNCTION: Binds to the constant Fc region of IgG with high  
affinity.  
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by  
an amide bond (Potential).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; M13825; AAA03664.1; -.  
DR PIR; A24496; A24496.  
DR PDB; 1EW7; X-ray; A=227-282.

DR PDB; 1FCC; X-ray; -.  
DR PDB; 1GB1; NMR; @=227-282.  
DR PDB; 1IGC; X-ray; A=292-352.  
DR PDB; 1IGD; X-ray; @=292-352.  
DR PDB; 1MPE; NMR; A/B/C/D=227-282.  
DR PDB; 1NVK; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=227-282.  
DR PDB; 1PGA; X-ray; @=227-282.  
DR PDB; 1PGB; X-ray; @=227-282.  
DR PDB; 1PGX; X-ray; @=284-366.  
DR PDB; 1Q10; NMR; A/B=227-282.  
DR PDB; 2GB1; NMR; @=227-282.  
DR PDB; 2IGD; X-ray; @=292-352.  
DR PDB; 2IGH; NMR; @=292-352.  
DR InterPro; IPR009063; Bac\_Ig\_alb\_bind.  
DR InterPro; IPR002988; GA.  
DR InterPro; IPR005877; Gpos\_Ysirk.  
DR InterPro; IPR001899; Gram\_pos\_anchor.  
DR InterPro; IPR000724; IgG\_bind\_B.  
DR Pfam; PF01468; GA; 2.  
DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR Pfam; PF01378; IgG binding B; 2.  
DR Pfam; PF04650; Ysirk signal; 1.  
DR PRINTS; PR00015; GPOSANCHOR.  
DR TIGRFAMs; TIGR01167; LPXTG\_anchor; 1.  
DR TIGRFAMs; TIGR01168; Ysirk signal; 1.  
DR PROSITE; PS00847; GRAM\_POS\_ANCHORING; 1.  
KW 3D-structure; Cell wall; IgG-binding protein; Peptidoglycan-anchor;  
KW Repeat; Signal.

FT SIGNAL 1 33  
FT CHAIN 34 417 Immunoglobulin G binding protein G.  
FT PROPEP 418 448 Removed by sortase (Potential).  
FT DOMAIN 69 111 Ala-rich.  
FT DOMAIN 104 215 2 X 37 AA repeats.  
FT REPEAT 104 140 1-1.  
FT REPEAT 179 215 1-2.  
FT DOMAIN 228 352 2 X 55 AA repeats.  
FT REPEAT 298 352 2-1.  
FT REPEAT 386 410 2-2.  
FT DOMAIN 414 418 5 X 5 AA repeats of [DE]-D-A-K-K.  
FT SITE 417 417 LPXTG sorting signal (Potential).  
FT MOD\_RES 417 417 Pentaglycyl murein peptidoglycan amidated  
threonine (Potential).  
FT STRAND 228 234  
FT STRAND 239 245  
FT HELIX 249 262  
FT TURN 263 264  
FT STRAND 268 272  
FT TURN 273 281  
FT STRAND 297 304  
FT STRAND 309 316  
FT HELIX 319 332  
FT TURN 333 334  
FT STRAND 338 342  
FT TURN 343 346  
FT STRAND 347 351  
SQ SEQUENCE 448 AA; 47567 MW; A0759060C8F9B6CA CRC64;

Query Match 83.6%; Score 281; DB 1; Length 448;  
Best Local Similarity 98.2%; Pred. No. 5e-23; Mismatches 0; Gaps 0;  
Matches 54; Conservative 0; Indels 1;

OY 3 TYKLINGTKLKGTTTAVDAATAEKVKFYQYANDNGVDGWTYYDDATKTFVTVE 57  
DB 228 TYKLINGTKLKGTTTAVDAATAEKVKFYQYANDNGVDGWTYYDDATKTFVTVE 282  
|||||

## RESULT 5

Q53337 PRELIMINARY; PRT; 60 AA.  
ID Q53337  
AC Q53337;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein G IgG Fc binding domain.
Name=FcFB;
OS Streptococcus sp. CMCC 32138.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=184480;
RN [1]
RP
RQ
Sequence from N.A.
RC STRAIN=CMCC 32138;
RC MEDLINE=93277681; PubMed=8503988;
RA Cai S.Y., Wang Y.Y., Yao Z.J.;
RT "Structure analysis of streptococcal protein G Fc binding domain.";
RL Sci. China, Ser. B, Chem. Life Sci. 36:75-80(1993).
DR EMBL; S62801; AAB27024.1; -.
DR HSSP; P19909; 1P7E.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01378; Igg_binding_B; 1.
SQ SEQUENCE 60 AA; 6655 MW; 924567E0D6B513DB CRC64;

Query Match 78.6%; Score 264; DB 2; Length 60;
Best Local Similarity 86.0%; Pred. No. 4.8e-22;
Matches 49; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57
Db 1 MTTVKLVINGKTLKGETTTKTVDATAETAKFAKQYANDNGVDGVWVTYDDATKTFVTVE 57

RESULT 6
Q53974 Q53974 PRELIMINARY; PRT; 413 AA.
AC Q53974;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mag protein precursor.
GN Name=mag;
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94259307; PubMed=7515368; DOI=10.1016/0378-1119(94)90609-2;
RA Jonsson H., Frykberg L., Rantamaeki L., Guss B.;
RT "MAG, a novel plasma protein receptor from Streptococcus dysgalactiae";
RL Gene 143:85-89(1994).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL; L27798; AAA26921.1; -.
DR PIR; S55890; S55890.
DR HSSP; P19909; 1P7E.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig_alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR01899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein G IgG Fc binding domain.
Name=FcFB;
OS Streptococcus sp. CMCC 32138.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=184480;
RN [1]
RP
RQ
Sequence from N.A.
RC STRAIN=CMCC 32138;
RC MEDLINE=93277681; PubMed=8503988;
RA Cai S.Y., Wang Y.Y., Yao Z.J.;
RT "Structure analysis of streptococcal protein G Fc binding domain.";
RL Sci. China, Ser. B, Chem. Life Sci. 36:75-80(1993).
DR EMBL; S62801; AAB27024.1; -.
DR HSSP; P19909; 1P7E.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01378; Igg_binding_B; 1.
SQ SEQUENCE 60 AA; 6655 MW; 924567E0D6B513DB CRC64;

Query Match 77.7%; Score 261; DB 2; Length 60;
Best Local Similarity 84.2%; Pred. No. 1.3e-20;
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57
Db 1 MTTVKLVINGKTLKGETTTKTVDATAETAKFAKQYANDNGVDGVWVTYDDATKTFVTVE 57

RESULT 8
Q53974 Q53974 PRELIMINARY; PRT; 413 AA.
AC Q53974;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mag protein precursor.
GN Name=mag;
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94192673; PubMed=8143736;
RA Jonsson H., Mueller H.P.;
RT "The type-III Fc receptor from Streptococcus dysgalactiae is also an alpha-2-macroglobulin receptor.";
RL Eur. J. Biochem. 220:819-826(1994).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL; Z29666; CAA82764.1; -.
DR PIR; S42574; S42574.
DR HSSP; P19909; 1P7E.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 5.
DR Pfam; PF04650; YSIRK_signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 664 surface protein.
SQ SEQUENCE 664 AA; 72023 MW; 4A41CEE7977862A CRC64;

Query Match 77.7%; Score 261; DB 2; Length 664;
Best Local Similarity 84.2%; Pred. No. 1.3e-20;
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57
Db 502 LTTVKLVINGKTLKGETTTKTVDATAETAKFAKQYANDNGVDGVWVTYDDATKTFVTVE 558

RESULT 8
Q93EM8 Q93EM8 PRELIMINARY; PRT; 669 AA.
ID Q93EM8
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AC Q93EM8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mig precursor.
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43078;
RX MEDLINE=21437603; PubMed=11553540;
RA DOI=10.1128/IAI.69.10.6030-6037.2001;
RA Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
RT "Surface-expressed mig protein protects Streptococcus dysgalactiae
RT against phagocytosis by bovine neutrophils.";
RL Infect. Immun. 69:6030-6037(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43078;
RA Song X.-M., Perez-Casal J., Potter A.A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AF354651; AAL09476.1; -
DR HSP; P19909; 1P7E.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg binding_B; 5.
DR Pfam; PF04650; Ysirk signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Cell wall; Peptidoglycan-anchor; -Signal.
FT SIGNAL 1 39 Potential.
FT CHAIN 40 669 Mig.
SQ SEQUENCE 669 AA; 72681 MW; 5C9982B952029B03 CRC64;

Query Match 76.5%; Score 257; DB 2; Length 669;
Best Local Similarity 82.5%; Pred. No. 3.8e-20;
Matches 47; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGETTAEVDAATAAKVFKQYANDNGVGDGEWYDDATKFTVTTE 57
Db 502 LTTYKLIVNGKTLKGETTTKAVDVETAERKAFQYANENGVDGVWYDDATKFTVTTE 558

RESULT 9
Q56212
ID Q56212 PRELIMINARY; PRT; 429 AA.
AC Q56212;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell surface protein precursor.
OS Streptococcus equi subsp. zooepidemicus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=40041;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=25;
RA Hong K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AB095372; BAD00711.1; -
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig_alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg binding_B; 2.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
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RA Jonsson H., Lindmark H., Guss B.;
RT "A protein G-related cell surface protein in Streptococcus
RT zooepidemicus.";
RL Infect. Immun. 63:2968-2975(1995).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; U25852; AAA86832.1; -
DR HSP; P06654; 2IGH.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig_alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg binding_B; 2.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; -Signal.
FT SIGNAL 1 33 Potential.
FT CHAIN 34 429 cell surface protein.
SQ SEQUENCE 429 AA; 44830 MW; 270D43F92C197BBA CRC64;

Query Match 65.5%; Score 220; DB 2; Length 429;
Best Local Similarity 70.2%; Pred. No. 3.3e-16;
Matches 40; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MTTYKLILNGKTLKGETTAEVDAATAAKVFKQYANDNGVGDGEWYDDATKFTVTTE 57
Db 298 LTTYRLVINGVTFSGTATKAVDAATAEQAFQYANDNGVVGWAYDAATKFTVTTE 354

RESULT 10
Q76K19
ID Q76K19 PRELIMINARY; PRT; 433 AA.
AC Q76K19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cell surface protein.
GN Name=tag;
OS Streptococcus equi subsp. zooepidemicus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=40041;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VTU211;
RA Hong K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; AB095372; BAD00711.1; -
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR009063; Bac_Ig_alb_bind.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF01468; GA; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg binding_B; 2.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
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DR TIGRFAMs; TIGR01168; YSIRK signal; 1.
KW PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anch.
SQ SEQUENCE 433 AA; 45386 MW; 22F27856AFD752D8 CRC64;

Query Match 65.5%; Score 220; DB 2; Length 433;
Best Local Similarity 68.4%; Pred. No. 3.3e-16;
Matches 39; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MTTVKLLNGKTLKGETTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTE 57
:||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 302 LTTVRLVIKGVTFSGSETAKVAATAEQTFQYANDNGITGEWAYDPAATKTFVTTE 358

RESULT 11
Q56192 PRELIMINARY; PRT; 573 AA.
AC Q56192;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BM3XM.
GN Name=pSBBM3XM;
OS Staphylococcus xyloso.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_taxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92325006; PubMed=1624418;
RA Hansson M., Stahl S., Nguyen T.N., Baechi T., Robert A., Binz H.,
RA Sjoelander A., Uhlen M.;
RT "Expression of recombinant proteins on the surface of the coagulase-
RT negative bacterium Staphylococcus xyloso.";
RL J. Bacteriol. 174:4239-4245(1992).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; M91198; AAA26599.1; -.
DR HSSP; P19909; 1GJT.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019865; F:immunoglobulin binding; IEA.
DR GO; GO:0016985; F:cell wall catabolism; IEA.
DR InterPro; IPR009063; Bac Ig/alb bind.
DR InterPro; IPR004829; Csurfact_antigen.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR005038; Octapeptide.
DR HSP; P19909; 1GJT.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019865; F:immunoglobulin binding; IEA.
DR GO; GO:0016985; F:cell wall catabolism; IEA.
DR InterPro; IPR009063; Bac Ig/alb bind.
DR InterPro; IPR004829; Csurfact_antigen.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR005038; Octapeptide.
DR Pfam; PF01468; GA; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 1.
DR Pfam; PF01476; LysM; 1.
DR Pfam; PF03373; Octapeptide; 13.
DR Pfam; PF04650; YSIRK_signal; 1.
DR ProDom; PD153432; Csurfact_antigen; 1.
DR SMART; SM00257; LysM; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anch.
SQ SEQUENCE 573 AA; 62133 MW; 81E0A458528AE24 CRC64;

Query Match 38.2%; Score 128.5; DB 2; Length 573;
Best Local Similarity 57.9%; Pred. No. 8.1e-06;
Matches 33; Conservative 1; Mismatches 18; Indels 5; Gaps 2;

Qy 3 TYKLINGKTLKGETTTTEAVDAATAAKV-FKQYANDNGVDGEWYDDATKTFVTTEH 58
|||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 TYKLINGKTLKGETTTTEAVDAATAARSPNFPILENSSSVPG---DPLESTCMVHEH 290

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RESULT 12
Q56193 PRELIMINARY; PRT; 492 AA.
AC Q56193;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BBXM.
GN Name=pSBBmp18XM;
OS Staphylococcus xyloso.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_taxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92325006; PubMed=1624418;
RA Hansson M., Stahl S., Nguyen T.N., Baechi T., Robert A., Binz H.,
RA Sjoelander A., Uhlen M.;
RT "Expression of recombinant proteins on the surface of the coagulase-
RT negative bacterium Staphylococcus xyloso.";
RL J. Bacteriol. 174:4239-4245(1992).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; M91199; AAA26600.1; -.
DR HSSP; P19909; 1GJT.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019865; F:immunoglobulin binding; IEA.
DR GO; GO:0016985; F:cell wall catabolism; IEA.
DR InterPro; IPR009063; Bac Ig/alb bind.
DR InterPro; IPR004829; Csurfact_antigen.
DR InterPro; IPR002988; GA.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR000724; Igg_bind_B.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR005038; Octapeptide.
DR Pfam; PF01468; GA; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF01378; Igg_binding_B; 1.
DR Pfam; PF01476; LysM; 1.
DR Pfam; PF03373; Octapeptide; 13.
DR Pfam; PF04650; YSIRK_signal; 1.
DR ProDom; PD153432; Csurfact_antigen; 1.
DR SMART; SM00257; LysM; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anch.
SQ SEQUENCE 492 AA; 52708 MW; 6581D37EED16952B CRC64;

Query Match 37.9%; Score 127.5; DB 2; Length 492;
Best Local Similarity 69.0%; Pred. No. 9e-06;
Matches 29; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

Qy 3 TYKLINGKTLKGETTTTEAVDAATAAKV-FKQYANDNGVDGE 43
|||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 TYKLINGKTLKGETTTTEAVDAATAARSPNFPILENSSSVPGD 279

RESULT 13
Q8RYL7 PRELIMINARY; PRT; 412 AA.
AC Q8RYL7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OSJNB0052012.3 protein (OSJNB0093F16.27 protein).
GN Name=OSJNB0052012.3; Synonyms=OSJNB0093F16.27;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Naniki N., Negishi M., Ohta I., Ono N., Sai S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AP004330; BAB90745.1; -.
DR EMBL; AP004332; BAB92907.1; -.
DR Gramene; Q8RYL7; -.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00888; HLH; 1.
SQ SEQUENCE 412 AA; 43142 MW; 5E3E2707EDA764E2 CRC64;

Query Match 22.3%; Score 75; DB 2; Length 412;
Best Local Similarity 38.8%; Pred. No. 5.7; Mismatches 5; Gaps 2;
Matches 19; Conservative 5;

Oy 20 EAVDAATAAKVFKQYANDNGVDGWY--DDATKTFVT--EHHHH 62
Db 34 EAEAAAAAKWDELAGGGGGGWSYLAADALAAASATPFFHHHH 82

RESULT 14
P73089
ID P73089 PRELIMINARY; PRT; 1965 AA.
AC P73089;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fat protein.
DE OrderedLocNames=srl2046;
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PCC6803;
MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Saito M., Saito K., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90903; BAA17114.1; -.
DR PIR; S75200; S75200.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR011121; W rich C.
DR Pfam; PF00028; Cadherin; 10.

DR Pfam; PF07483; W rich C; 2.
DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM00112; CA; 10.
DR PROSITE; PS0268; CADHERIN_2; 10.
KW Complete proteome.
SQ SEQUENCE 1965 AA; 205730 MW; BC536EDAB1747C78 CRC64;

Query Match 22.0%; Score 74; DB 2; Length 1965;
Best Local Similarity 32.1%; Pred. No. 39;
Matches 18; Conservative 16; Mismatches 16; Indels 6; Gaps 2;

Oy 3 TYKLLNGKTLKGETTTEAV--DAATAKVKQYANDNGVDGWYDDATKTFVT 56
Db 148 THTIIINGSQLQVEQSVQSLGESVTNVNRP----TGSGSDGSPFDLFTQTFVT 199

RESULT 15
Q7N736
ID Q7N736 PRELIMINARY; PRT; 148 AA.
AC Q7N736;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferric uptake transcription regulator (Ferric uptake regulator).
DE Name=fur; OrderedLocNames=plu1327;
OS Photobacterium luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photobacterium.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TT01;
MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguler P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photobacterium
RT luminescens";
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571863; CAE13620.1; -.
DR HSSP; Q03456; IMZB.
DR Photolista; plu1327; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002481; FUR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01475; FUR; 1.
DR ProDom; PD02003; FUR; 1.
KW Complete proteome.
SQ SEQUENCE 148 AA; 16979 MW; EBF62F7673B00207 CRC64;

Query Match 20.5%; Score 69; DB 2; Length 148;
Best Local Similarity 29.8%; Pred. No. 9;
Matches 17; Conservative 9; Mismatches 21; Indels 10; Gaps 2;

Oy 5 KLIINGKTLKGETTTEAVDAATAKVKQYANDNGVDGWYDDATKTFVTTEHHH 61
Db 42 KLIDNG-----EIGLATVTVRLNQF--DDAGIVTRHNFEGKSVFELTQHHH 88

Search completed: August 9, 2005, 10:20:24
Job time : 177 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2005, 10:10:50 ; Search time 39 Seconds  
(without alignments)  
152.960 Million cell updates/sec

Title: US-10-672-108-6  
Perfect score: 336  
Sequence: 1 MTTVKLILNGKTLKGETTTE.....EWTYDDATKTFVTVEHHHH 62

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285	84.8	455	A45063	immunoglobulin-bin
2	284	84.5	593	S00128	protein G precursor
3	281	83.6	448	A24496	IGG-binding protei
4	261	77.7	413	S55890	plasma protein rec
5	261	77.7	664	S42574	streptococcal surf
6	74	22.0	1965	S75200	fat protein - Syne
7	68	20.2	1020	D83679	hypothetical prote
8	64.5	19.2	148	S70733	ferric uptake tran
9	64.5	19.2	148	AE0321	ferric uptake regu
10	64.5	19.2	737	S14408	translation elonga
11	64	19.0	1081	T31094	surface antigen Bs
12	63.5	18.9	308	H81345	hypothetical prote
13	63	18.8	148	D83973	hypothetical prote
14	63	18.8	1347	T30909	endo-1,4-beta-xyla
15	62.5	18.6	148	S90718	negative regulator
16	62.5	18.6	148	S07308	ferric uptake tran
17	62.5	18.6	148	B85568	negative regulator
18	62.5	18.6	150	AB0586	ferric uptake regu
19	62.5	18.6	260	T18909	hypothetical prote
20	62.5	18.6	296	T40267	outer surface prot
21	61.5	18.3	640	A41726	homeotic protein B
22	61.5	18.3	642	S27806	homeotic protein B
23	61.5	18.3	736	S31809	translation elonga
24	61.5	18.3	1156	T23308	hypothetical prote
25	61	18.2	148	G83681	urease accessory p
26	61	18.2	248	A12703	prokaryotic type I
27	61	18.2	248	A97486	prokaryotic type I
28	61	18.2	831	T00323	chitinase (EC 3.2
29	61	18.2	1902	B45764	lactocepin (EC 3.4

ALIGNMENTS

RESULT 1

A45063  
immunoglobulin-binding protein LG - Peptostreptococcus magnus  
C:Species: Peptostreptococcus magnus  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Oct-1999  
C:Accession: A45063  
R:Kihlberg, B.M.; Sjobring, U.; Kastern, W.; Bjorck, L.  
J. Biol. Chem. 267, 25583-25588, 1992  
A:Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties.  
A:Reference number: A45063; MUID:93094283; PMID:1460053  
A:Accession: A45063  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-455 <KH>  
A:Cross-references: GB:S50809; NID:G261705; PIDN:AAA03280.1; PID:G261706  
A:Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBI:120303)  
Query Match 84.8%; Score 285; DB 2; Length 455;  
Best Local Similarity 96.5%; Pred. No. 3e-24;  
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MTTVKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEMTYDDATKTFVTVE 57  
Db 328 MDTVKLILNGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEMTYDDATKTFVTVE 384

RESULT 2

S00128  
protein G precursor - Streptococcus sp. (Streptococcus G148)  
N:Alternate names: albumin-binding protein; cell wall-bound protein  
C:Species: Streptococcus sp.  
A:Variety: Streptococcus G148  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: S00128; A27604; A26314  
R:Olsson, A.; Eliasson, M.; Guss, B.; Nilsson, B.; Hellman, U.; Lindberg, M.; Uhlen, M.  
Eur. J. Biochem. 168, 319-324, 1987  
A:Title: Structure and evolution of the repetitive gene encoding streptococcal protein (endo-1,4-beta-xylanase) from Streptococcus G148  
A:Reference number: S00128; MUID:88029445; PMID:3663928  
A:Accession: S00128  
A:Molecule type: DNA  
A:Residues: 1-593 <OLS>  
A:Cross-references: UNIPROT:P19909; EMBL:X06173; NID:G47084; PIDN:CAA29540.1; PID:G4708  
A:Note: the source is designated as Streptococcus G148  
A:Note: part of this sequence, including the amino end of the mature protein, was confi.  
R:Sjobring, U.; Falkenberg, C.; Nielsen, E.; Akerstrom, B.; Bjorck, L.  
J. Immunol. 140, 1595-1599, 1988  
A:Title: Isolation and characterization of a 14-kDa albumin-binding fragment of strepto  
A:Reference number: A27604; MUID:88154455; PMID:2831269  
A:Accession: A27604  
A:Molecule type: protein  
A:Residues: 62-101 <SJO>  
R:Guss, B.; Eliasson, M.; Olsson, A.; Uhlen, M.; Frej, A.K.; Jorvall, H.; Flock, J.I.;

EMBO J. 5, 1567-1575, 1986  
A:Title: Structure of the IgG-binding regions of streptococcal protein G.  
A:Reference number: A26314; MUID:86300657; PMID:3017704  
A:Accession: A26314  
A:Molecule type: DNA  
A:Residues: 114-593 <GUS>  
A:Cross-references: GB:X04015; NID:g47071; PIDN:CAA27638.1; PID:g47072  
C:Function:  
A:Description: it is part of the cell wall structure of group G streptococci and is cov  
C:Superfamily: M5 protein  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:34-593/Product: protein G #status experimental <MAT>  
F:34-116/Domain: alanine-rich <ALA>  
F:117-290/Domain: AB duplication <DUPL>  
F:117-140/Region: A repeat  
F:141-191/Region: B  
F:192-215/Region: A repeat  
F:216-266/Region: B  
F:267-280/Region: A repeat  
F:303-497/Domain: IGG binding <IGB>  
F:303-357/Region: C repeat  
F:358-372/Region: D  
F:373-427/Region: C repeat  
F:428-442/Region: C repeat  
F:443-497/Region: C repeat  
F:498-567/Domain: proline-rich <PRO>  
F:568-593/Domain: carboxyl-terminal <CTD>  
  
Query Match 84.5%; Score 284; DB 2; Length 593;  
Best Local Similarity 93.0%; Pred. No. 5.2e-24;  
Matches 53; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 MTTYKLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 371 VTTYKLINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGWTYDDATKTFVTVE 427  
  
RESULT 3  
A24496  
IGG-binding protein - Streptococcus sp. (group G)  
C:Species: Streptococcus sp.  
C:Date: 17-Sep-1987 #sequence\_revision 17-Sep-1987 #text\_change 09-Jul-2004  
A:Accession: A24496; A39041  
R:Faehnestock, S.R.; Alexander, P.; Nagle, J.; Filpula, D.  
J. Bacteriol. 167, 870-880, 1986  
A:Title: Gene for an immunoglobulin-binding protein from a group G Streptococcus.  
A:Reference number: A24496; MUID:86304178; PMID:3745123  
A:Accession: A24496  
A:Molecule type: DNA  
A:Residues: 1-448 <FAH>  
A:Cross-references: UNIPROT:P06654; GB:M13825; NID:g153822; PIDN:AAA03664.1; PID:g153823  
R:Sjoeborg, U.; Bjoerck, L.; Kastern, W.  
J. Biol. Chem. 266, 399-405, 1991  
A:Title: Streptococcal protein G. Gene structure and protein binding properties.  
A:Reference number: A39041; MUID:91093154; PMID:1985908  
A:Accession: A39041  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 34-42, 'N', 45-48; 62-76; 186-200 <SUO>  
C:Genetics:  
A:Gene: spg  
C:Superfamily: M5 protein  
C:Keywords: transmembrane protein  
  
Query Match 83.6%; Score 281; DB 2; Length 448;  
Best Local Similarity 98.2%; Pred. No. 8.3e-24;  
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 TYKLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 228 TYKLINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGWTYDDATKTFVTVE 282

## RESULT 4

S55890  
plasma protein receptor MAG precursor - Streptococcus dysgalactiae  
C:Species: Streptococcus dysgalactiae  
C:Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S55890  
R:Jonsson, H.; Frykberg, L.; Rantamaeki, L.; Guss, B.  
Gene 143, 85-89, 1994  
A:Title: MAG, a novel plasma protein receptor from Streptococcus dysgalactiae.  
A:Reference number: S55890; MUID:94259307; PMID:7515368  
A:Accession: S55890  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-413 <JON>  
A:Cross-references: UNIPROT:Q53974; EMBL:L27798; NID:g475117; PIDN:AAA26921.1; PID:g4751  
C:Superfamily: M5 protein  
  
Query Match 77.7%; Score 261; DB 2; Length 413;  
Best Local Similarity 84.2%; Pred. No. 1.3e-21;  
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MTTYKLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 256 LTTYKLINGKTLKGETTTEAVDAATAEKAFKQYANENGVDGWTYDDATKTFVTVE 312  
  
RESULT 5  
S42574  
streptococcal surface protein - Streptococcus dysgalactiae  
C:Species: Streptococcus dysgalactiae  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S42574  
R:Jonsson, H.; Mueller, H.P.  
Eur. J. Biochem. 220, 819-826, 1994  
A:Title: The type-III FC receptor from Streptococcus dysgalactiae is also an alpha(2)-ma  
A:Reference number: S42574; MUID:94192673; PMID:8143736  
A:Accession: S42574  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-664 <JON>  
A:Cross-references: UNIPROT:Q53975; EMBL:Z29666; NID:g470220; PIDN:CAA82764.1; PID:g4702  
C:Superfamily: M5 protein  
  
Query Match 77.7%; Score 261; DB 2; Length 664;  
Best Local Similarity 84.2%; Pred. No. 2.2e-21;  
Matches 48; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 MTTYKLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTVE 57  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 502 LTTYKLINGKTLKGETTTEAVDAATAEKAFKQYANENGVDGWTYDDATKTFVTVE 558  
  
RESULT 6  
S75200  
fat protein - Synecocystis sp. (strain PCC 6803)  
A:Alternate names: protein slr2046  
C:Species: Synecocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S75200  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S75200  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1965 <KAN>  
A:Cross-references: UNIPROT:P73089; EMBL:D90903; GB:AB001339; NID:g1652127; PIDN:BAAI711  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996



A;Cross-references: UNIPROT:Q99718; GB:BA000018; PID:g13701654; PIDN:BAB42947.1; GSPDB: C;Experimental source: strain N315  
A;Genetics: C;Gene: SA1678  
C;Superfamily: ferric uptake regulator

Query Match 18.8%; Score 63; DB 2; Length 148;  
Best Local Similarity 38.2%; Pred. No. 7.1;  
Matches 13; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

QY 29 KVFQYANDGVGDGWTYYDDATKTFVTVEHHH 62  
DB 70 RVFK----DIGIVKELTYGDSSSRDFDNTHYH 99

RESULT 14

T30909  
endo-1,4-beta-xylanase (EC 3.2.1.8) - Caldocellum saccharolyticum  
C;Species: Caldocellum saccharolyticum  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30909  
R;Te'o Jr., V.S.; Gibbs, M.D.; Saul, D.J.; Bergquist, P.L.  
submitted to the EMBL Data Library, May 1997  
A;Reference number: Z20932  
A;Accession: T30909  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1347 <TEO>  
A;Cross-references: UNIPROT:Q30426; EMBL:AF005383; NID:g2645411; PID:g2645416; PIDN:AAB8  
C;Genetics: C;Gene: XynF  
C;Keywords: glycosidase; hydrolase  
F;1244-1340/Domain: Clostridium xylanase A repeat homology <CXA>

Query Match 18.8%; Score 63; DB 2; Length 1347;  
Best Local Similarity 30.6%; Pred. No. 82;  
Matches 19; Conservative 11; Mismatches 18; Indels 14; Gaps 3;

QY 4 YKLILNGKTLGETTTEAVDAA-----TAAKVFQYANDGVGDGWTYYDDATKTFV 55  
DB 436 YKAVRVYKVGPDTKETFLAAKITSNGKESYQELIKGFANKN---EWT--SISGTFI 489

QY 56 TE 57  
DB 490 SQ 491

RESULT 15

B90718  
negative regulator [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: B90718  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: B90718  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-148 <HAY>  
A;Cross-references: UNIPROT:P06975; GB:BA000007; PIDN:BAB34137.1; PID:g13360172; GSPDB: C;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics: C;Gene: ECS0714  
C;Superfamily: ferric uptake regulator

Query Match 18.6%; Score 62.5; DB 2; Length 148;  
Best Local Similarity 28.6%; Pred. No. 8.1;  
Matches 12; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 20 EAVDAATAAKVFQYANDGVGDGWTYYDDATKTFVTVEHHH 61

Db 48 BEIGLATVYRVLNQF-DDAGIVTRHNFEGGKSVFELTQQHH 88

Search completed: August 9, 2005, 10:21:08  
Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2005, 10:07:30 ; Search time 161 Seconds  
(without alignments)  
148.939 Million cell updates/sec

Title: US-10-672-108-6  
Perfect score: 336  
Sequence: 1 MTTVKLILNGTKLGETTE.....EWYDDATKTFVTEHHHH 62

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 16Dec04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	100.0	62	4 AAB30886	Aab30886 Amino aci
2	332	98.8	62	4 AAB30894	Aab30894 Amino aci
3	331	98.5	62	4 AAB30925	Aab30925 Amino aci
4	331	98.5	62	4 AAB30926	Aab30926 Amino aci
5	331	98.5	62	4 AAB30883	Aab30883 Amino aci
6	326	97.0	62	4 AAB30885	Aab30885 Amino aci
7	325	96.7	62	4 AAB30891	Aab30891 Amino aci
8	325	96.7	62	4 AAB30888	Aab30888 Amino aci
9	325	96.7	62	4 AAB30887	Aab30887 Amino aci
10	323	96.1	62	4 AAB30884	Aab30884 Amino aci
11	323	96.1	62	4 AAB30890	Aab30890 Amino aci
12	323	96.1	62	4 AAB30889	Aab30889 Amino aci
13	317	94.3	62	4 AAB30892	Aab30892 Amino aci
14	317	94.3	62	4 AAB30893	Aab30893 Amino aci
15	285	84.8	434	2 AAR42994	Aar42994 Sequence
16	284	84.5	61	2 AAW44390	Aaw44390 Protein G
17	284	84.5	64	2 AAW44395	Aaw44395 Protein G
18	284	84.5	78	2 AAR11382	Aar11382 FC-bindin
19	284	84.5	78	2 AAR11383	Aar11383 FC-bindin
20	284	84.5	185	3 AAY57610	Aay57610 Streptoco
21	284	84.5	228	3 AAB10433	Aab10433 Expressio
22	284	84.5	250	3 AAB10434	Aab10434 Expressio
23	284	84.5	269	2 AAR53295	Aar53295 Igg-bindi
24	284	84.5	402	2 AAW21716	Aaw21716 RIP fusio
25	284	84.5	402	2 AAW25129	Aaw25129 Pro-ribos

26	284	84.5	480	1	AAP70468	Aap70468 Sequence
27	284	84.5	489	2	AAR20085	Aar20085 Maize RIP
28	284	84.5	489	2	AAW21717	Aaw21717 RIP fusio
29	284	84.5	489	2	AAW25130	Aaw25130 Pro-ribos
30	284	84.5	493	2	AAW21719	Aaw21719 RIP fusio
31	284	84.5	493	2	AAW25132	Aaw25132 Pro-ribos
32	284	84.5	502	2	AAW21720	Aaw21720 RIP fusio
33	284	84.5	502	2	AAW25133	Aaw25133 Pro-ribos
34	284	84.5	593	2	AAR62944	Aar62944 Streptoco
35	282	83.9	607	2	AAR91016	Aar91016 PRSVPGLU
36	282	83.9	611	2	AAR91018	Aar91018 PRSVPGLU
37	281	83.6	55	6	ABR43647	Ab43647 Streptoco
38	281	83.6	55	8	ADO39742	Ado39742 Protein G
39	281	83.6	55	8	ADR49519	Adr49519 Staphyloc
40	281	83.6	55	8	ADR49521	Adr49521 Streptoco
41	281	83.6	56	4	AAE07440	Aae07440 Streptoco
42	281	83.6	56	6	ABU12183	Abu12183 Immunoglo
43	281	83.6	57	2	AAW44389	Aaw44389 Protein G
44	281	83.6	131	1	AAP94791	Aap94791 Protein G
45	281	83.6	131	2	AAR07008	Aar07008 Protein G

ALIGNMENTS

RESULT 1  
AAB30886  
ID AAB30886 standard; protein; 62 AA.

AC AAB30886;  
XX  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a B1 domain of protein G with mutation E27A.  
XX  
XX B1 domain; protein G; Fab fragment; immunoglobulin G; IGG; Fc fragment;  
KW knobs-into-holes binding site.  
XX  
OS Synthetic.  
OS Streptococcus sp.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 28 /note= "Glu changed to Ala"  
FT  
XX  
XX WO200074728-A1.  
XX  
XX 14-DEC-2000.

XX  
XX 02-JUN-2000; 2000WO-US015366.  
XX  
PR 04-JUN-1999; 99US-00326342.  
XX  
XX (UYDU-) UNIV DUKE.  
XX  
XX Hellinga HW, Sloan DJ;  
XX  
XX WPI; 2001-049994/06.  
XX  
XX N-PSDB; AAC86821.

XX  
XX B1 domain polypeptide of bacterial protein G, useful for detection and purification of antibody fragments, exhibits binding activity for Fab fragment of an Igg but does not bind Fc fragment.

XX  
PS Claim 7; Page 73; 83pp; English.

XX  
XX The present sequence represents a mutated B1 domain of the bacterial protein G. The B1 domain exhibits binding activity for a Fab fragment of an immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment of an Igg. The B1 domain may further comprise a disrupted or mutated "knobs-into-holes" binding site for a Fc fragment of an Igg. The Glu27 residue of the mature B1 domain acts as a charged knob on the surface of the B1 domain, inserting a polar hole on the Fc fragment. A

CC mutation of this residue virtually abolishes stable complex formation.  
 CC The B1 domain can be immobilized to a solid phase support, and be used  
 CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate  
 CC by affinity chromatography. The B1 domain is also useful for detecting  
 CC IgG or its fragments in a clinical sample  
 XX  
 SQ Sequence 62 AA;

Query Match 100.0%; Score 336; DB 4; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-34;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTEHHH 60  
 Db 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTEHHH 60

Oy 61 HH 62  
 ||  
 Db 61 HH 62

## RESULT 2

AAB30894  
 ID AAB30894 standard; protein; 62 AA.

AC AAB30894;

DT 02-APR-2001 (first entry)

XX Amino acid sequence of a mutated B1 domain of protein G.

DE B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;  
 KW knobs-into-holes binding site.

XX Synthetic.

OS Streptococcus sp.

XX WO200074728-A1.

PD 14-DEC-2000.

XX 02-JUN-2000; 2000WO-US015366.

XX 04-JUN-1999; 99US-00326342.

XX (UYDU-) UNIV DUKE.

PI Hellinga HW, Sloan DJ;

DR WPI; 2001-049994/06.

XX N-PSDB; AAC86827.

XX B1 domain polypeptide of bacterial protein G, useful for detection and  
 PT purification of antibody fragments, exhibits binding activity for Fab  
 PT fragment of an IgG but does not bind Fc fragment.

PS Claim 7; Page 79; 83pp; English.

XX The present sequence represents a mutated B1 domain of the bacterial  
 CC protein G. The B1 domain exhibits binding activity for a Fab fragment  
 CC of an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
 CC fragment of an IgG. The B1 domain may further comprise a disrupted or  
 CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The  
 CC Glu27 residue of the mature B1 domain acts as a charged knob on the  
 CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
 CC mutation of this residue virtually abolishes stable complex formation.  
 CC The B1 domain can be immobilized to a solid phase support, and be used  
 CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate  
 CC by affinity chromatography. The B1 domain is also useful for detecting  
 CC IgG or its fragments in a clinical sample

XX Sequence 62 AA;

Query Match 98.8%; Score 332; DB 4; Length 62;  
 Best Local Similarity 98.4%; Pred. No. 1.4e-33;  
 Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTEHHH 60  
 Db 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTEHHH 60

Oy 61 HH 62  
 ||  
 Db 61 HH 62

## RESULT 3

AAB30925  
 ID AAB30925 standard; protein; 62 AA.

XX AAB30925;

XX 02-APR-2001 (first entry)

XX Amino acid sequence of a mutated B1 domain of protein G.

DE B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;  
 KW knobs-into-holes binding site.

XX Synthetic.

OS Streptococcus sp.

XX WO200074728-A1.

PD 14-DEC-2000.

XX 02-JUN-2000; 2000WO-US015366.

XX 04-JUN-1999; 99US-00326342.

XX (UYDU-) UNIV DUKE.

PI Hellinga HW, Sloan DJ;

DR WPI; 2001-049994/06.

XX N-PSDB; AAC86828.

XX B1 domain polypeptide of bacterial protein G, useful for detection and  
 PT purification of antibody fragments, exhibits binding activity for Fab  
 PT fragment of an IgG but does not bind Fc fragment.

PS Claim 7; Page 80; 83pp; English.

XX The present sequence represents a mutated B1 domain of the bacterial  
 CC protein G. The B1 domain exhibits binding activity for a Fab fragment of  
 CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
 CC fragment of an IgG. The B1 domain may further comprise a disrupted or  
 CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The  
 CC Glu27 residue of the mature B1 domain acts as a charged knob on the  
 CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
 CC mutation of this residue virtually abolishes stable complex formation.  
 CC The B1 domain can be immobilized to a solid phase support, and be used  
 CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate  
 CC by affinity chromatography. The B1 domain is also useful for detecting  
 CC IgG or its fragments in a clinical sample

XX Sequence 62 AA;

Query Match 98.5%; Score 331; DB 4; Length 62;  
 Best Local Similarity 98.4%; Pred. No. 1.9e-33;  
 Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTEHHH 60  
 Db 1 MTTVKLLINGKTLKGETTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKTFVTTEHHH 60



QY 61 HH 62  
DB 61 HH 62

## RESULT 4

AAB30926  
ID AAB30926 standard; protein; 62 AA.

XX AAB30926;

XX 02-APR-2001 (first entry)

XX Amino acid sequence of a mutated B1 domain of protein G.

XX B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;  
XX knobs-into-holes binding site.

XX Synthetic.

OS Streptococcus sp.

XX WO200074728-A1.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-US015366.

XX 04-JUN-1999; 99US-00326342.

XX (UYDU-) UNIV DUKE.

XX Hellinga HW, Sloan DJ;

XX WPI; 2001-049994/06.

DR N-PSDB; AAC86829.

XX B1 domain polypeptide of bacterial protein G, useful for detection and  
XX purification of antibody fragments, exhibits binding activity for Fab  
XX fragment of an Igg but does not bind Fc fragment.

XX Claim 7; Page 81; 83pp; English.

XX The present sequence represents a mutated B1 domain of the bacterial  
XX protein G. The B1 domain exhibits binding activity for a Fab fragment of  
XX an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
XX fragment of an Igg. The B1 domain may further comprise a disrupted or  
XX mutated "knobs-into-holes" binding site for a Fc fragment of an Igg. The  
XX Glu27 residue of the mature B1 domain acts as a charged knob on the  
XX surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
XX mutation of this residue virtually abolishes stable complex formation.  
XX The B1 domain can be immobilized to a solid phase support, and be used  
XX for purifying Fc and Fab fragments of Igg from a warm-blooded vertebrate  
XX by affinity chromatography. The B1 domain is also useful for detecting  
XX Igg or its fragments in a clinical sample

XX Sequence 62 AA;

Query Match 98.5%; Score 331; DB 4; Length 62;

Best Local Similarity 98.4%; Pred. No. 1.9e-33;

Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTTTKLIILNGKTLKGETTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60  
DB 1 MTTTKLIILNGKTLKGETTTTEAVDAATAIKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60

QY 61 HH 62

DB 61 HH 62

## RESULT 5

AAB30883  
ID AAB30883 standard; protein; 62 AA.

XX  
AC  
DT

02-APR-2001 (first entry)

XX Amino acid sequence of the native B1 domain of protein G.

XX B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;  
XX knobs-into-holes binding site.

OS Streptococcus sp.

XX Key Location/Qualifiers

FT Protein 2..62

FT /note= "mature protein"

PN WO200074728-A1.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-US015366.

XX 04-JUN-1999; 99US-00326342.

XX (UYDU-) UNIV DUKE.

XX Hellinga HW, Sloan DJ;

XX WPI; 2001-049994/06.

DR N-PSDB; AAC86820.

XX B1 domain polypeptide of bacterial protein G, useful for detection and  
XX purification of antibody fragments, exhibits binding activity for Fab  
XX fragment of an Igg but does not bind Fc fragment.

XX Disclosure; Page 50; 83pp; English.

XX The present sequence represents a native B1 domain of the bacterial  
XX protein G. The B1 domain exhibits binding activity for a Fab fragment of  
XX an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
XX fragment of an Igg. The B1 domain may further comprise a disrupted or  
XX mutated "knobs-into-holes" binding site for a Fc fragment of an Igg. The  
XX Glu27 residue of the mature B1 domain acts as a charged knob on the  
XX surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
XX mutation of this residue virtually abolishes stable complex formation.  
XX The B1 domain can be immobilized to a solid phase support, and be used  
XX for purifying Fc and Fab fragments of Igg from a warm-blooded vertebrate  
XX by affinity chromatography. The B1 domain is also useful for detecting  
XX Igg or its fragments in a clinical sample

XX Sequence 62 AA;

Query Match 98.5%; Score 331; DB 4; Length 62;

Best Local Similarity 98.4%; Pred. No. 1.9e-33;

Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTTTKLIILNGKTLKGETTTTEAVDAATAAKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60  
DB 1 MTTTKLIILNGKTLKGETTTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKFTVTEHHH 60

QY 61 HH 62

DB 61 HH 62

## RESULT 6

AAB30885  
ID AAB30885 standard; protein; 62 AA.

XX AAB30885;

XX 02-APR-2001 (first entry)

DE	Amino acid sequence of a B1 domain of protein G with mutation T25A.
XX	
KW	B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW	knobs-into-holes binding site.
XX	
OS	Synthetic.
OS	Streptococcus sp.
XX	
Key	Location/Qualifiers
FH	2. .62
FT	/note= "mature protein"
FT	Misc-difference 26
FT	/note= "wild type Thr changed to Ala"
XX	
PN	WC0200074728-A1.
PD	14-DEC-2000.
XX	
Pf	02-JUN-2000; 200WO-US015366.
PR	04-JUN-1999; 99US-00326342.
XX	
PA	(UYDU-) UNIV DUKE.
PI	Hellingsa HW, Sloan DJ;
PI	WPI; 2001-049994/06.
DR	
XX	
PT	B1 domain polypeptide of bacterial protein G, useful for detection and purification of antibody fragments, exhibits binding activity for Fab fragment of an Igg but does not bind Fc fragment.
XX	
PS	Example 1; Page 72; 83pp; English.
XX	
CC	The present sequence represents a mutated B1 domain of the bacterial protein G. The B1 domain exhibits binding activity for a Fab fragment of an immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment of an Igg. The B1 domain may further comprise a disrupted or mutated "knoBs-into-holes" binding site for a Fc fragment of an Igg. The Glu28 residue of the B1 domain acts as a charged knob on the surface of the B1 domain, inserting a polar hole on the Fc fragment. A mutation of this residue virtually abolishes stable complex formation. The B1 domain can be immobilized to a solid phase support, and be used for purifying Fc and Fab fragments of Igg from a warm-blooded vertebrate by affinity chromatography. The B1 domain is also useful for detecting Igg or its fragments in a clinical sample
XX	
SQ	Sequence 62 AA;
	Query Match 97.0%; Score 326; DB 4; Length 62;
	Best Local Similarity 96.8%; Pred. No. 7.9e-33;
	Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 MTTVKILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEWTYDDATKTFTVTEHHH 60 
Dd	1 MTTVKILNGKTLKGTTTEAVDAAAEEKVFKQYANDNGVDGEWTYDDATKTFTVTEHHH 60 
Qy	61 HH 62 
Dd	61 HH 62
RESULT 7	
AAB30891	
ID	AAB30891 standard; protein; 62 AA.
XX	
AC	AAB30891;
XX	
DT	02-APR-2001 (first entry)
XX	
DE	Amino acid sequence of a B1 domain of protein G with mutation E42A.
XX	
KW	B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;



PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-US015366.  
 XX  
 PR 04-JUN-1999; 99US-00326342.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Hellinga HW, Sloan DJ;  
 XX  
 DR WPI; 2001-049994/06.  
 XX  
 PT B1 domain polypeptide of bacterial protein G, useful for detection and  
 XX purification of antibody fragments, exhibits binding activity for Fab  
 XX fragment of an Igg but does not bind Fc fragment.  
 XX  
 PS Example 1; Page 72; 83pp; English.  
 XX  
 CC The present sequence represents a mutated B1 domain of the bacterial  
 CC protein G. The B1 domain exhibits binding activity for a Fab fragment of  
 CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
 CC fragment of an Igg. The B1 domain may further comprise a disrupted or  
 CC mutated "knobs-into-holes" binding site for a Fc fragment of an Igg. The  
 CC Glu28 residue of the B1 domain acts as a charged knob on the surface of  
 CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of  
 CC this residue virtually abolishes stable complex formation. The B1 domain  
 CC can be immobilized to a solid phase support, and be used for purifying Fc  
 CC and Fab fragments of Igg from a warm-blooded vertebrate by affinity  
 CC chromatography. The B1 domain is also useful for detecting Igg or its  
 CC fragments in a clinical sample  
 XX  
 SQ Sequence 62 AA;  
 Query Match 96.1%; Score 323; DB 4; Length 62;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-32;  
 Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MTTVKILNGKTLGKETTTEAVDAATAKVKQYANDNGVDGWTYDDATKTFVTTEHHH 60  
 DB 1 MTTVKILNGKTLGKETTTEAVDAATAKVKQYANDNGVDGWTYDDATKTFVTTEHHH 60  
 QY 61 HH 62  
 DB 61 HH 62  
 RESULT 11  
 AAB30890  
 ID AAB30890 standard; protein; 62 AA.  
 XX  
 AC AAB30890;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of a B1 domain of protein G with mutation D40A.  
 XX  
 KW B1 domain; protein G; Fab fragment; immunoglobulin G; Igg; Fc fragment;  
 XX knobs-into-holes binding site.  
 OS Synthetic.  
 OS Streptococcus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 41 /note= "Asp changed to Ala"  
 FT  
 XX WO200074728-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-US015366.  
 XX  
 PR 04-JUN-1999; 99US-00326342.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Hellinga HW, Sloan DJ;  
 XX

XX (UYDU-) UNIV DUKE.  
 XX  
 PI Hellinga HW, Sloan DJ;  
 XX  
 DR WPI; 2001-049994/06.  
 XX  
 PT B1 domain polypeptide of bacterial protein G, useful for detection and  
 XX purification of antibody fragments, exhibits binding activity for Fab  
 XX fragment of an Igg but does not bind Fc fragment.  
 XX  
 PS Disclosure; Page 76; 83pp; English.  
 XX  
 CC The present sequence represents a mutated B1 domain of the bacterial  
 CC protein G. The B1 domain exhibits binding activity for a Fab fragment of  
 CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
 CC fragment of an Igg. The B1 domain may further comprise a disrupted or  
 CC mutated "knobs-into-holes" binding site for a Fc fragment of an Igg. The  
 CC Glu27 residue of the mature B1 domain acts as a charged knob on the  
 CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
 CC mutation of this residue virtually abolishes stable complex formation.  
 CC The B1 domain can be immobilized to a solid phase support, and be used  
 CC for purifying Fc and Fab fragments of Igg from a warm-blooded vertebrate  
 CC by affinity chromatography. The B1 domain is also useful for detecting  
 CC Igg or its fragments in a clinical sample  
 XX  
 SQ Sequence 62 AA;  
 Query Match 96.1%; Score 323; DB 4; Length 62;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-32;  
 Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MTTVKILNGKTLGKETTTEAVDAATAKVKQYANDNGVDGWTYDDATKTFVTTEHHH 60  
 DB 1 MTTVKILNGKTLGKETTTEAVDAATAKVKQYANDNGVDGWTYDDATKTFVTTEHHH 60  
 QY 61 HH 62  
 DB 61 HH 62  
 RESULT 12  
 AAB30889  
 ID AAB30889 standard; protein; 62 AA.  
 XX  
 AC AAB30889;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of a B1 domain of protein G with mutation N35A.  
 XX  
 KW B1 domain; protein G; Fab fragment; immunoglobulin G; Igg; Fc fragment;  
 XX knobs-into-holes binding site.  
 OS Synthetic.  
 OS Streptococcus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 35 /note= "Asn changed to Ala"  
 FT  
 XX WO200074728-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-US015366.  
 XX  
 PR 04-JUN-1999; 99US-00326342.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Hellinga HW, Sloan DJ;  
 XX

DR WPI; 2001-049994/06.  
 DR N-PSDB; AAC86824.  
 XX B1 domain polypeptide of bacterial protein G, useful for detection and  
 PT purification of antibody fragments, exhibits binding activity for Fab  
 PT fragment of an IgG but does not bind Fc fragment.  
 XX Claim 7; Page 76; 83pp; English.  
 XX The present sequence represents a mutated B1 domain of the bacterial  
 CC protein G. The B1 domain exhibits binding activity for a Fab fragment of  
 CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
 CC fragment of an IgG. The B1 domain may further comprise a disrupted or  
 CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The  
 CC Glu27 residue of the mature B1 domain acts as a charged knob on the  
 CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
 CC mutation of this residue virtually abolishes stable complex formation.  
 CC The B1 domain can be immobilized to a solid phase support, and be used  
 CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate  
 CC by affinity chromatography. The B1 domain is also useful for detecting  
 CC IgG or its fragments in a clinical sample  
 XX Sequence 62 AA;  
 SQ

Query Match 96.1%; Score 323; DB 4; Length 62;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-32;  
 Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MTTTKYLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEYDDATKTFVTVEHHH 60  
 DB 1 MTTTKYLILNGKTLKGTTTEAVDAATAEKVFKQYAADNGVDGEYDDATKTFVTVEHHH 60  
 QY 61 HH 62  
 DB 61 HH 62

RESULT 13  
 AAB30892  
 ID AAB30892 standard; protein; 62 AA.  
 AC AAB30892;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of a B1 domain of protein G with mutation W43A.  
 XX  
 KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;  
 KW knobs-into-holes binding site.  
 XX  
 OS Synthetic.  
 OS Streptococcus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 44 /note= "Trp changed to Ala"  
 FT  
 XX WO200074728-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-US015366.  
 XX  
 PR 04-JUN-1999; 99US-00326342.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Hellinga HW, Sloan DJ;  
 XX  
 DR WPI; 2001-049994/06.  
 DR N-PSDB; AAC86825.  
 XX  
 PT B1 domain polypeptide of bacterial protein G, useful for detection and

PT purification of antibody fragments, exhibits binding activity for Fab  
 PT fragment of an IgG but does not bind Fc fragment.  
 XX Claim 23; Page 77; 83pp; English.  
 XX The present sequence represents a mutated B1 domain of the bacterial  
 CC protein G. The B1 domain exhibits binding activity for a Fab fragment of  
 CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc  
 CC fragment of an IgG. The B1 domain may further comprise a disrupted or  
 CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The  
 CC Glu27 residue of the mature B1 domain acts as a charged knob on the  
 CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A  
 CC mutation of this residue virtually abolishes stable complex formation.  
 CC The B1 domain can be immobilized to a solid phase support, and be used  
 CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate  
 CC by affinity chromatography. The B1 domain is also useful for detecting  
 CC IgG or its fragments in a clinical sample  
 XX Sequence 62 AA;  
 SQ

Query Match 94.3%; Score 317; DB 4; Length 62;  
 Best Local Similarity 96.8%; Pred. No. 1e-31;  
 Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MTTTKYLILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGEYDDATKTFVTVEHHH 60  
 DB 1 MTTTKYLILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEYDDATKTFVTVEHHH 60  
 QY 61 HH 62  
 DB 61 HH 62

RESULT 14  
 AAB30893  
 ID AAB30893 standard; protein; 62 AA.  
 XX  
 AC AAB30893;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of a B1 domain of protein G with mutation T44A/Y45A.  
 XX  
 KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;  
 KW knobs-into-holes binding site.  
 XX  
 OS Synthetic.  
 OS Streptococcus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 45 /note= "Thr changed to Ala"  
 FT  
 FT Misc-difference 46 /note= "Tyr changed to Ala"  
 FT  
 XX WO200074728-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-US015366.  
 XX  
 PR 04-JUN-1999; 99US-00326342.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Hellinga HW, Sloan DJ;  
 XX  
 DR WPI; 2001-049994/06.  
 DR N-PSDB; AAC86826.  
 XX  
 PT B1 domain polypeptide of bacterial protein G, useful for detection and  
 PT purification of antibody fragments, exhibits binding activity for Fab  
 PT fragment of an IgG but does not bind Fc fragment.

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XX PS Claim 27; Page 78; 83pp; English.
XX CC The present sequence represents a mutated B1 domain of the bacterial
XX CC protein G. The B1 domain exhibits binding activity for a Fab fragment of
XX CC an immunoglobulin (Ig) G but exhibits no binding activity for a Fc
XX CC fragment of an IgG. The B1 domain may further comprise a disrupted or
XX CC mutated "knobs-into-holes" binding site for a Fc fragment of an IgG. The
XX CC Glu27 residue of the mature B1 domain acts as a charged knob on the
XX CC surface of the B1 domain, inserting a polar hole on the Fc fragment. A
XX CC mutation of this residue virtually abolishes stable complex formation.
XX CC The B1 domain can be immobilized to a solid phase support, and be used
XX CC for purifying Fc and Fab fragments of IgG from a warm-blooded vertebrate
XX CC by affinity chromatography. The B1 domain is also useful for detecting
XX CC IgG or its fragments in a clinical sample
XX SQ Sequence 62 AA;
    Query Match          94.3%; Score 317; DB 4; Length 62;
    Best Local Similarity 95.2%; Pred. No. 1e-31;
    Matches 59; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MTTVKLIILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTTEHHH 60
Db 1 MTTVKLIILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWAADATKTFVTTEHHH 60
Qy 61 HH 62
Db 61 HH 62
RESULT 15
AAR42994
ID AAR42994 standard; protein; 434 AA.
XX AC AAR42994;
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 16-MAY-1994 (first entry)
XX DE Sequence encoding immunoglobulin light chain binding protein.
XX KW Immunoglobulin; light chain; binding; identification; purification;
XX KW separation; ss.
XX OS Escherichia coli.
XX FH Key Location/Qualifiers
FT Domain 5..305
FT /label= B1 immunoglobulin light chain binding domain.
FT Domain 81..305
FT /label= B2 immunoglobulin light chain binding domain.
FT Domain 153..305
FT /label= B3 immunoglobulin light chain binding domain.
FT Domain 225..305
FT /label= B4 immunoglobulin light chain binding domain.
FT Domain 297..305
FT /label= B5 immunoglobulin light chain binding domain.
FT Domain 309..434
FT /label= C1 immunoglobulin heavy chain binding domain.
FT Domain 364..434
FT /label= D intermediate immunoglobulin heavy chain binding
FT Domain 379..434
FT /label= C2 immunoglobulin heavy chain binding domain.
XX WO9322342-A1.
XX PD 11-NOV-1993.
XX PF 28-APR-1993; 93WO-SE000375.
XX
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28-APR-1992; 92SE-00001331.  
(HIGH-) HIGHTECH RECEPTOR AB.  
Bjoerck L, Sjoebbring U;  
WPI; 1993-368722/46.  
P-PSDB; AAR42994.  
New protein L binding light chains of all immunoglobulin classes - for  
binding purifying and identifying immunoglobulin, also related DNA,  
vectors and host cells.  
Claim 6; Page 39-40; 71pp; English.  
Protein L (AAR42993) is capable of binding to immunoglobulin G light  
chains. It is useful for binding, separating (purifying) and identifying  
immunoglobulin and for removing immunoglobulin molecules from serum. This  
is the coding sequence of one hybrid protein of the L protein. The hybrid  
proteins can bind all human immunoglobulin classes and many  
immunoglobulins from other species. They are highly soluble and retain  
their binding activity at high temperatures over a pH range of 3-10. They  
can be immobilised without loss of activity. (Updated on 25-MAR-2003 to  
correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)  
SQ Sequence 434 AA;  
Query Match 84.8%; Score 285; DB 2; Length 434;  
Best Local Similarity 96.5%; Pred. No. 1.2e-26;  
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MTTVKLIILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTTE 57  
Db 307 MDTYKLIILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKTFVTTE 363  
Search completed: August 9, 2005, 10:17:23  
Job time : 163 secs

28-APR-1992; 92SE-00001331.  
(HIGH-) HIGHTECH RECEPTOR AB.  
Bjoerck L, Sjoebbring U;  
WPI; 1993-368722/46.  
P-PSDB; AAR42994.  
New protein L binding light chains of all immunoglobulin classes - for  
binding purifying and identifying immunoglobulin, also related DNA,  
vectors and host cells.  
Claim 6; Page 39-40; 71pp; English.  
Protein L (AAR42993) is capable of binding to immunoglobulin G light  
chains. It is useful for binding, separating (purifying) and identifying  
immunoglobulin and for removing immunoglobulin molecules from serum. This  
is the coding sequence of one hybrid protein of the L protein. The hybrid  
proteins can bind all human immunoglobulin classes and many  
immunoglobulins from other species. They are highly soluble and retain  
their binding activity at high temperatures over a pH range of 3-10. They  
can be immobilised without loss of activity. (Updated on 25-MAR-2003 to  
correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)  
SQ Sequence 434 AA;  
Query Match 84.8%; Score 285; DB 2; Length 434;  
Best Local Similarity 96.5%; Pred. No. 1.2e-26;  
Matches 55; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MTTVKLIILNGKTLKGTTTEAVDAATAAKVFKQYANDNGVDGWTYDDATKTFVTTE 57  
Db 307 MDTYKLIILNGKTLKGTTTEAVDAATAEKVFKQYANDNGVDGEWYDDATKTFVTTE 363  
Search completed: August 9, 2005, 10:17:23  
Job time : 163 secs